



SEQUENCE LISTING

<110> Lu, Shan
Shen, Siyuan

<120> COMPOSITIONS AND METHODS FOR CYTOMEGALOVIRUS TREATMENT

<130> 07917-190001

<140> US 10/789,247

<141> 2004-02-27

<150> US 60/450,818

<151> 2003-02-27

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<213> Human cytomegalovirus

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gtc	tgt	ctg	ggc	gct	gcg	gtt	tcc	tct	tct	agt	act	tcc	cat	gca	act	96
Val	Cys	Leu	Gly	Ala	Ala	Val	Ser	Ser	Ser	Ser	Thr	Ser	His	Ala	Thr	
		20					25					30				

tct	tct	act	cac	aat	gga	agc	cat	act	tct	cgt	acg	acg	tct	gct	caa	144
Ser	Ser	Thr	His	Asn	Gly	Ser	His	Thr	Ser	Arg	Thr	Thr	Ser	Ala	Gln	
		35				40						45				

acc	cgg	tca	gtc	tat	tct	caa	cac	gta	acg	tct	tct	gaa	gcc	gtc	agt	192
Thr	Arg	Ser	Val	Tyr	Ser	Gln	His	Val	Thr	Ser	Ser	Glu	Ala	Val	Ser	
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cat	aga	gcc	aac	gag	act	atc	tac	aac	act	acc	ctc	aag	tac	gga	gat	240
His	Arg	Ala	Asn	Glu	Thr	Ile	Tyr	Asn	Thr	Thr	Leu	Lys	Tyr	Gly	Asp	
65				70					75					80		

gtg	gtg	gga	gtc	aac	act	acc	aag	tac	ccc	tat	cgc	gtg	tgt	tct	atg	288
Val	Val	Gly	Val	Asn	Thr	Thr	Lys	Tyr	Pro	Tyr	Arg	Val	Cys	Ser	Met	
			85						90					95		

gcc	cag	ggc	acg	gat	ctt	att	cgc	ttt	gaa	cgt	aat	atc	atc	tgc	acc	336
Ala	Gln	Gly	Thr	Asp	Leu	Ile	Arg	Phe	Glu	Arg	Asn	Ile	Ile	Cys	Thr	
			100					105						110		

tcg atg aag cct atc aat gaa gac ttg gat gag ggc atc atg gtg gtc Ser Met Lys Pro Ile Asn Glu Asp Leu Asp Glu Gly Ile Met Val Val 115 120 125	384
tac aag cgc aac atc gtg gcg cac acc ttt aag gta cgg gtc tac caa Tyr Lys Arg Asn Ile Val Ala His Thr Phe Lys Val Arg Val Tyr Gln 130 135 140	432
aag gtt ttg acg ttt cgt cgt agc tac gct tac atc tac acc act tat Lys Val Leu Thr Phe Arg Arg Ser Tyr Ala Tyr Ile Tyr Thr Thr Tyr 145 150 155 160	480
ctg ctg ggc agc aat acg gaa tac gtg gcg cct cct atg tgg gag att Leu Leu Gly Ser Asn Thr Glu Tyr Val Ala Pro Pro Met Trp Glu Ile 165 170 175	528
cat cac atc aac aag ttt gct caa tgc tac agt tcc tac agc cgc gtt His His Ile Asn Lys Phe Ala Gln Cys Tyr Ser Ser Tyr Ser Arg Val 180 185 190	576
ata gga ggc acg gtt ttc gtg gca tat cat agg gac agt tat gaa aac Ile Gly Gly Thr Val Phe Val Ala Tyr His Arg Asp Ser Tyr Glu Asn 195 200 205	624
aaa acc atg caa tta att ccc gac gat tat tcc aac acc cac agt acc Lys Thr Met Gln Leu Ile Pro Asp Asp Tyr Ser Asn Thr His Ser Thr 210 215 220	672
cgt tac gtg acg gtc aag gat cag tgg cac agc cgc ggc agc acc tgg Arg Tyr Val Thr Val Lys Asp Gln Trp His Ser Arg Gly Ser Thr Trp 225 230 235 240	720
ctc tat cgt gag acc tgt aat ctg aac tgt atg ctg acc atc act act Leu Tyr Arg Glu Thr Cys Asn Leu Asn Cys Met Leu Thr Ile Thr Thr 245 250 255	768
gcg cgc tcc aag tat cct tat cat ttt ttt gca act tcc acg ggt gat Ala Arg Ser Lys Tyr Pro Tyr His Phe Phe Ala Thr Ser Thr Gly Asp 260 265 270	816
gtg gtt tac att tct cct ttc tac aac gga acc aat cgc aat gcc agc Val Val Tyr Ile Ser Pro Phe Tyr Asn Gly Thr Asn Arg Asn Ala Ser 275 280 285	864
tac ttt gga gaa aac gcc gac aag ttt ttc att ttc ccg aac tac acc Tyr Phe Gly Glu Asn Ala Asp Lys Phe Phe Ile Phe Pro Asn Tyr Thr 290 295 300	912
atc gtt tcc gac ttt gga aga ccc aac gct gcg cca gaa acc cat agg Ile Val Ser Asp Phe Gly Arg Pro Asn Ala Ala Pro Glu Thr His Arg 305 310 315 320	960
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cag gac gag aag aat gtc acc tgc cag ctc acc ttc tgg gaa gcc tcg Gln Asp Glu Lys Asn Val Thr Cys Gln Leu Thr Phe Trp Glu Ala Ser 340 345 350	1056
gaa cgt act atc cgt tcc gaa gcc gaa gac tcg tac cac ttt tct tct Glu Arg Thr Ile Arg Ser Glu Ala Glu Asp Ser Tyr His Phe Ser Ser 355 360 365	1104
gcc aaa atg act gca act ttt ctg tct aag aaa caa gaa gtg aac atg Ala Lys Met Thr Ala Thr Phe Leu Ser Lys Lys Gln Glu Val Asn Met 370 375 380	1152
tcc gac tcc gcg ctg gac tgc gta cgt gat gag gct ata aat aag tta Ser Asp Ser Ala Leu Asp Cys Val Arg Asp Glu Ala Ile Asn Lys Leu 385 390 395 400	1200
cag cag att ttc aat act tca tac aat caa aca tat gaa aaa tac gga Gln Gln Ile Phe Asn Thr Ser Tyr Asn Gln Thr Tyr Glu Lys Tyr Gly 405 410 415	1248
aac gtg tcc gtc ttc gaa acc agc ggc ggt ctg gtg gtg ttc tgg caa Asn Val Ser Val Phe Glu Thr Ser Gly Gly Leu Val Val Phe Trp Gln 420 425 430	1296
ggc atc aag caa aaa tct ttg gtg gaa ttg gaa cgt ttg gcc aat cga Gly Ile Lys Gln Lys Ser Leu Val Glu Leu Glu Arg Leu Ala Asn Arg 435 440 445	1344
tcc agt ctg aat atc act cat agg acc aga aga agt acg agt gac aat Ser Ser Leu Asn Ile Thr His Arg Thr Arg Arg Ser Thr Ser Asp Asn 450 455 460	1392
aat aca act cat ttg tcc agc atg gaa tcg gtg cac aat ctg gtc tac Asn Thr Thr His Leu Ser Ser Met Glu Ser Val His Asn Leu Val Tyr 465 470 475 480	1440
gcc cag ctg cag ttc acc tat gac acg ttg cgc ggt tac atc aac cgg Ala Gln Leu Gln Phe Thr Tyr Asp Thr Leu Arg Gly Tyr Ile Asn Arg 485 490 495	1488
gcg ctg gcg caa atc gca gaa gcc tgg tgt gtg gat caa cgg cgc acc Ala Leu Ala Gln Ile Ala Glu Ala Trp Cys Val Asp Gln Arg Arg Thr 500 505 510	1536
cta gag gtc ttc aag gaa ctc agc aag atc aac ccg tca gcc att ctc Leu Glu Val Phe Lys Glu Leu Ser Lys Ile Asn Pro Ser Ala Ile Leu 515 520 525	1584
tcg gcc att tac aac aaa ccg att gcc gcg cgt ttc atg ggt gat gtc Ser Ala Ile Tyr Asn Lys Pro Ile Ala Ala Arg Phe Met Gly Asp Val 530 535 540	1632
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ctg cgt gat atg aac gtg aag gaa tcg cca gga cgc tgc tac tca cga	1728

Leu	Arg	Asp	Met	Asn	Val	Lys	Glu	Ser	Pro	Gly	Arg	Cys	Tyr	Ser	Arg	
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ccc	gtg	gtc	atc	ttt	aat	ttc	gcc	aac	agc	tcg	tac	gtg	cag	tac	ggc	1776
Pro	Val	Val	Ile	Phe	Asn	Phe	Ala	Asn	Ser	Ser	Tyr	Val	Gln	Tyr	Gly	
			580					585					590			
caa	ctg	ggc	gag	gac	aac	gaa	atc	ctg	ttg	ggc	aac	cac	cgc	act	gag	1824
Gln	Leu	Gly	Glu	Asp	Asn	Glu	Ile	Leu	Leu	Gly	Asn	His	Arg	Thr	Glu	
		595					600					605				
gaa	tgt	cag	ctt	ccc	agc	ctc	aag	atc	ttc	atc	gcc	ggg	aac	tcg	gcc	1872
Glu	Cys	Gln	Leu	Pro	Ser	Leu	Lys	Ile	Phe	Ile	Ala	Gly	Asn	Ser	Ala	
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Tyr	Glu	Tyr	Val	Asp	Tyr	Leu	Phe	Lys	Arg	Met	Ile	Asp	Leu	Ser	Ser	
	625				630					635					640	
atc	tcc	acc	gtc	gac	agc	atg	atc	gcc	ctg	gat	atc	gac	ccg	ctg	gaa	1968
Ile	Ser	Thr	Val	Asp	Ser	Met	Ile	Ala	Leu	Asp	Ile	Asp	Pro	Leu	Glu	
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aat	acc	gac	ttc	agg	gta	ctg	gaa	ctt	tac	tcg	cag	aaa	gag	ctg	cgt	2016
Asn	Thr	Asp	Phe	Arg	Val	Leu	Glu	Leu	Tyr	Ser	Gln	Lys	Glu	Leu	Arg	
			660					665					670			
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Ser	Ser	Asn	Val	Phe	Asp	Leu	Glu	Glu	Ile	Met	Arg	Glu	Phe	Asn	Ser	
		675					680					685				
tac	aag	cag	cgg	gta	aag	tac	gtg	gag	gac	aag	gta	gtc	gac	ccg	cta	2112
Tyr	Lys	Gln	Arg	Val	Lys	Tyr	Val	Glu	Asp	Lys	Val	Val	Asp	Pro	Leu	
	690						695				700					
ccg	ccc	tac	ctc	aag	ggc	ctg	gac	gac	ctc	atg	agc	ggc	ctg	ggc	gcc	2160
Pro	Pro	Tyr	Leu	Lys	Gly	Leu	Asp	Asp	Leu	Met	Ser	Gly	Leu	Gly	Ala	
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Ala	Gly	Lys	Ala	Val	Gly	Val	Ala	Ile	Gly	Ala	Val	Gly	Gly	Ala	Val	
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gcc	tcc	gtg	gtc	gaa	ggc	gtt	gcc	acc	ttc	ctc	aaa	aac	ccc	ttc	gga	2256
Ala	Ser	Val	Val	Glu	Gly	Val	Ala	Thr	Phe	Leu	Lys	Asn	Pro	Phe	Gly	
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gcc	ttc	acc	atc	atc	ctc	gtg	gcc	ata	gcc	gta	gtc	att	atc	act	tat	2304
Ala	Phe	Thr	Ile	Ile	Leu	Val	Ala	Ile	Ala	Val	Val	Ile	Ile	Thr	Tyr	
		755					760					765				
ttg	atc	tat	act	cga	cag	cgg	cgt	ctg	tgc	acg	cag	ccg	ctg	cag	aac	2352
Leu	Ile	Tyr	Thr	Arg	Gln	Arg	Arg	Leu	Cys	Thr	Gln	Pro	Leu	Gln	Asn	
	770					775					780					
ctc	ttt	ccc	tat	ctg	gtg	tcc	gcc	gac	ggg	acc	acc	gtg	acg	tcg	ggc	2400
Leu	Phe	Pro	Tyr	Leu	Val	Ser	Ala	Asp	Gly	Thr	Thr	Val	Thr	Ser	Gly	

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agc acc aaa gac acg tcg tta cag gct ccg cct tcc tac gag gaa agt				2448
Ser Thr Lys Asp Thr Ser Leu Gln Ala Pro Pro Ser Tyr Glu Glu Ser	805	810	815	
gtt tat aat tct ggt cgc aaa gga ccg gga cca ccg tcg tct gat gca				2496
Val Tyr Asn Ser Gly Arg Lys Gly Pro Gly Pro Pro Ser Ser Asp Ala	820	825	830	
tcc acg gcg gct ccg cct tac acc aac gag cag gct tac cag atg ctt				2544
Ser Thr Ala Ala Pro Pro Tyr Thr Asn Glu Gln Ala Tyr Gln Met Leu	835	840	845	
ctg gcc ctg gcc cgt ctg gac gca gag cag cga gcg cag cag aac ggt				2592
Leu Ala Leu Ala Arg Leu Asp Ala Glu Gln Arg Ala Gln Gln Asn Gly	850	855	860	
aca gat tct ttg gac gga cag act ggc acg cag gac aag gga cag aag				2640
Thr Asp Ser Leu Asp Gly Gln Thr Gly Thr Gln Asp Lys Gly Gln Lys	865	870	875	880
cct aac ctg cta gac cgg ctg cga cat cgc aaa aac ggc tac aga cac				2688
Pro Asn Leu Leu Asp Arg Leu Arg His Arg Lys Asn Gly Tyr Arg His	885	890	895	
ttg aaa gac tcc gac gaa gaa gag aac gtc tga				2721
Leu Lys Asp Ser Asp Glu Glu Glu Asn Val	900	905		

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<212> PRT

<213> Human cytomegalovirus

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Ser Ser Thr His Asn Gly Ser His Thr Ser Arg Thr Thr Ser Ala Gln	35	40	45	
Thr Arg Ser Val Tyr Ser Gln His Val Thr Ser Ser Glu Ala Val Ser	50	55	60	
His Arg Ala Asn Glu Thr Ile Tyr Asn Thr Thr Leu Lys Tyr Gly Asp	65	70	75	80
Val Val Gly Val Asn Thr Thr Lys Tyr Pro Tyr Arg Val Cys Ser Met	85	90	95	
Ala Gln Gly Thr Asp Leu Ile Arg Phe Glu Arg Asn Ile Ile Cys Thr	100	105	110	
Ser Met Lys Pro Ile Asn Glu Asp Leu Asp Glu Gly Ile Met Val Val	115	120	125	
Tyr Lys Arg Asn Ile Val Ala His Thr Phe Lys Val Arg Val Tyr Gln	130	135	140	
Lys Val Leu Thr Phe Arg Arg Ser Tyr Ala Tyr Ile Tyr Thr Thr Tyr	145	150	155	160

Leu	Leu	Gly	Ser	Asn	Thr	Glu	Tyr	Val	Ala	Pro	Pro	Met	Trp	Glu	Ile	
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His	His	Ile	Asn	Lys	Phe	Ala	Gln	Cys	Tyr	Ser	Ser	Tyr	Ser	Arg	Val	
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Ile	Gly	Gly	Thr	Val	Phe	Val	Ala	Tyr	His	Arg	Asp	Ser	Tyr	Glu	Asn	
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Lys	Thr	Met	Gln	Leu	Ile	Pro	Asp	Asp	Tyr	Ser	Asn	Thr	His	Ser	Thr	
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Arg	Tyr	Val	Thr	Val	Lys	Asp	Gln	Trp	His	Ser	Arg	Gly	Ser	Thr	Trp	
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Leu	Tyr	Arg	Glu	Thr	Cys	Asn	Leu	Asn	Cys	Met	Leu	Thr	Ile	Thr	Thr	
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Ala	Arg	Ser	Lys	Tyr	Pro	Tyr	His	Phe	Phe	Ala	Thr	Ser	Thr	Gly	Asp	
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Val	Val	Tyr	Ile	Ser	Pro	Phe	Tyr	Asn	Gly	Thr	Asn	Arg	Asn	Ala	Ser	
	275						280					285				
Tyr	Phe	Gly	Glu	Asn	Ala	Asp	Lys	Phe	Phe	Ile	Phe	Pro	Asn	Tyr	Thr	
	290					295					300					
Ile	Val	Ser	Asp	Phe	Gly	Arg	Pro	Asn	Ala	Ala	Pro	Glu	Thr	His	Arg	
305					310					315					320	
Leu	Val	Ala	Phe	Leu	Glu	Arg	Ala	Asp	Ser	Val	Ile	Ser	Trp	Asp	Ile	
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Gln	Asp	Glu	Lys	Asn	Val	Thr	Cys	Gln	Leu	Thr	Phe	Trp	Glu	Ala	Ser	
			340					345					350			
Glu	Arg	Thr	Ile	Arg	Ser	Glu	Ala	Glu	Asp	Ser	Tyr	His	Phe	Ser	Ser	
	355					360					365					
Ala	Lys	Met	Thr	Ala	Thr	Phe	Leu	Ser	Lys	Lys	Gln	Glu	Val	Asn	Met	
	370					375					380					
Ser	Asp	Ser	Ala	Leu	Asp	Cys	Val	Arg	Asp	Glu	Ala	Ile	Asn	Lys	Leu	
385				390						395					400	
Gln	Gln	Ile	Phe	Asn	Thr	Ser	Tyr	Asn	Gln	Thr	Tyr	Glu	Lys	Tyr	Gly	
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Asn	Val	Ser	Val	Phe	Glu	Thr	Ser	Gly	Gly	Leu	Val	Val	Phe	Trp	Gln	
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Gly	Ile	Lys	Gln	Lys	Ser	Leu	Val	Glu	Leu	Glu	Arg	Leu	Ala	Asn	Arg	
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Ser	Ser	Leu	Asn	Ile	Thr	His	Arg	Thr	Arg	Arg	Ser	Thr	Ser	Asp	Asn	
	450					455					460					
Asn	Thr	Thr	His	Leu	Ser	Ser	Met	Glu	Ser	Val	His	Asn	Leu	Val	Tyr	
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Ala	Gln	Leu	Gln	Phe	Thr	Tyr	Asp	Thr	Leu	Arg	Gly	Tyr	Ile	Asn	Arg	
			485						490					495		
Ala	Leu	Ala	Gln	Ile	Ala	Glu	Ala	Trp	Cys	Val	Asp	Gln	Arg	Arg	Thr	
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Leu	Glu	Val	Phe	Lys	Glu	Leu	Ser	Lys	Ile	Asn	Pro	Ser	Ala	Ile	Leu	
	515					520						525				
Ser	Ala	Ile	Tyr	Asn	Lys	Pro	Ile	Ala	Ala	Arg	Phe	Met	Gly	Asp	Val	
	530				535						540					
Leu	Gly	Leu	Ala	Ser	Cys	Val	Thr	Ile	Asn	Gln	Thr	Ser	Val	Lys	Val	
545				550						555					560	
Leu	Arg	Asp	Met	Asn	Val	Lys	Glu	Ser	Pro	Gly	Arg	Cys	Tyr	Ser	Arg	
			565						570					575		
Pro	Val	Val	Ile	Phe	Asn	Phe	Ala	Asn	Ser	Ser	Tyr	Val	Gln	Tyr	Gly	
			580					585					590			
Gln	Leu	Gly	Glu	Asp	Asn	Glu	Ile	Leu	Leu	Gly	Asn	His	Arg	Thr	Glu	
	595					600						605				
Glu	Cys	Gln	Leu	Pro	Ser	Leu	Lys	Ile	Phe	Ile	Ala	Gly	Asn	Ser	Ala	

610		615		620	
Tyr Glu Tyr Val Asp	Tyr Leu Phe Lys Arg Met	Ile Asp Leu Ser Ser			
625	630	635	640		
Ile Ser Thr Val Asp	Ser Met Ile Ala Leu Asp	Ile Asp Pro Leu Glu			
	645	650	655		
Asn Thr Asp Phe Arg	Val Leu Glu Leu Tyr Ser	Gln Lys Glu Leu Arg			
	660	665	670		
Ser Ser Asn Val Phe Asp	Leu Glu Ile Met Arg	Glu Phe Asn Ser			
	675	680	685		
Tyr Lys Gln Arg Val Lys	Tyr Val Glu Asp Lys	Val Val Asp Pro Leu			
	690	695	700		
Pro Pro Tyr Leu Lys Gly	Leu Asp Asp Leu Met Ser	Gly Leu Gly Ala			
705	710	715	720		
Ala Gly Lys Ala Val Gly	Val Ala Ile Gly Ala	Val Gly Gly Ala Val			
	725	730	735		
Ala Ser Val Val Glu Gly	Val Ala Thr Phe Leu Lys	Asn Pro Phe Gly			
	740	745	750		
Ala Phe Thr Ile Ile Leu	Val Ala Ile Ala Val	Val Ile Ile Thr Tyr			
	755	760	765		
Leu Ile Tyr Thr Arg Gln	Arg Arg Leu Cys Thr	Gln Pro Leu Gln Asn			
	770	775	780		
Leu Phe Pro Tyr Leu Val	Ser Ala Asp Gly Thr	Thr Val Thr Ser Gly			
785	790	795	800		
Ser Thr Lys Asp Thr Ser	Leu Gln Ala Pro	Pro Ser Tyr Glu Glu Ser			
	805	810	815		
Val Tyr Asn Ser Gly Arg	Lys Gly Pro Gly	Pro Pro Ser Ser Asp Ala			
	820	825	830		
Ser Thr Ala Ala Pro Pro	Tyr Thr Asn Glu Gln	Ala Tyr Gln Met Leu			
	835	840	845		
Leu Ala Leu Ala Arg Leu	Asp Ala Glu Gln Arg	Ala Gln Gln Asn Gly			
	850	855	860		
Thr Asp Ser Leu Asp Gly	Gln Thr Gly Thr Gln	Asp Lys Gly Gln Lys			
865	870	875	880		
Pro Asn Leu Leu Asp Arg	Leu Arg His Arg Lys	Asn Gly Tyr Arg His			
	885	890	895		
Leu Lys Asp Ser Asp Glu	Glu Glu Glu Asn Val				
	900	905			

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tct atc gtt ttc atg gtg ctg act ttt gtc aac gtc agc gtg cat cta	96
Ser Ile Val Phe Met Val Leu Thr Phe Val Asn Val Ser Val His Leu	
20 25 30	
gtg ctg agc aat ttt ccg cac ctg ggc tac ccc tgc gtc tac tat cac	144

Val	Leu	Ser	Asn	Phe	Pro	His	Leu	Gly	Tyr	Pro	Cys	Val	Tyr	Tyr	His	
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gtc	gtg	gac	ttt	gaa	agg	ctc	aac	atg	tcg	gcc	tac	aac	gta	atg	cac	192
Val	Val	Asp	Phe	Glu	Arg	Leu	Asn	Met	Ser	Ala	Tyr	Asn	Val	Met	His	
	50					55				60						
ctg	cac	acg	cct	atg	ctt	ttc	tta	gac	tcg	gtg	cag	ttg	gtg	tgc	tac	240
Leu	His	Thr	Pro	Met	Leu	Phe	Leu	Asp	Ser	Val	Gln	Leu	Val	Cys	Tyr	
65					70				75					80		
gcc	gtg	ttc	atg	cag	ctc	gtc	ttt	tta	gcc	gtg	acc	atc	tac	tac	ctg	288
Ala	Val	Phe	Met	Gln	Leu	Val	Phe	Leu	Ala	Val	Thr	Ile	Tyr	Tyr	Leu	
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gta	tgc	tgg	atc	aag	atc	agc	atg	cgc	aag	gac	aaa	ggc	atg	agc	cta	336
Val	Cys	Trp	Ile	Lys	Ile	Ser	Met	Arg	Lys	Asp	Lys	Gly	Met	Ser	Leu	
			100					105					110			
aac	cag	tcg	aca	cgc	gac	att	tcg	tac	atg	ggc	gac	agc	ctc	aca	gcc	384
Asn	Gln	Ser	Thr	Arg	Asp	Ile	Ser	Tyr	Met	Gly	Asp	Ser	Leu	Thr	Ala	
		115					120					125				
ttc	ctc	ttc	att	ctc	agc	atg	gac	acg	ttc	caa	cta	ttc	aca	ctg	acc	432
Phe	Leu	Phe	Ile	Leu	Ser	Met	Asp	Thr	Phe	Gln	Leu	Phe	Thr	Leu	Thr	
	130					135					140					
atg	tca	ttt	cgg	ctg	ccc	agc	atg	atc	gcc	ttc	atg	gcc	gcc	gtg	cac	480
Met	Ser	Phe	Arg	Leu	Pro	Ser	Met	Ile	Ala	Phe	Met	Ala	Ala	Val	His	
145					150				155					160		
ttt	ttc	tgc	ctg	acc	att	ttc	aac	gtg	agc	atg	gtc	acg	cag	tac	cgc	528
Phe	Phe	Cys	Leu	Thr	Ile	Phe	Asn	Val	Ser	Met	Val	Thr	Gln	Tyr	Arg	
			165					170					175			
agc	tac	aaa	cgc	tca	ctc	ttt	ttc	ttc	tcg	cgt	ctg	cac	ccc	aag	ctc	576
Ser	Tyr	Lys	Arg	Ser	Leu	Phe	Phe	Phe	Ser	Arg	Leu	His	Pro	Lys	Leu	
			180					185					190			
aaa	ggt	acg	gtg	cag	ttc	cgc	acg	ctc	atc	gtc	aac	ctg	gta	gag	gta	624
Lys	Gly	Thr	Val	Gln	Phe	Arg	Thr	Leu	Ile	Val	Asn	Leu	Val	Glu	Val	
		195					200					205				
gcg	ctt	ggt	ttc	aac	acc	acc	gtg	gta	gcc	atg	gcc	ctg	tgc	tac	ggc	672
Ala	Leu	Gly	Phe	Asn	Thr	Thr	Val	Val	Ala	Met	Ala	Leu	Cys	Tyr	Gly	
	210					215					220					
ttc	gga	aac	aac	ttt	ttc	gtg	cgt	aca	ggc	cac	atg	gtg	tta	gcc	gtc	720
Phe	Gly	Asn	Asn	Phe	Phe	Val	Arg	Thr	Gly	His	Met	Val	Leu	Ala	Val	
225					230				235					240		
ttc	gtg	gtc	tac	gct	atc	atc	tcc	atc	atc	tac	ttt	tta	ctg	atc	gag	768
Phe	Val	Val	Tyr	Ala	Ile	Ile	Ser	Ile	Ile	Tyr	Phe	Leu	Leu	Ile	Glu	
				245				250						255		
gcc	gtc	ttt	ttt	caa	tac	gtc	aag	gtg	caa	ttc	ggc	tac	cac	ctg	ggc	816
Ala	Val	Phe	Phe	Gln	Tyr	Val	Lys	Val	Gln	Phe	Gly	Tyr	His	Leu	Gly	

260	265	270	
gcc ttc ttt gga ctc tgc ggc ctc atc tac ccc atc gtg cag tac gat			864
Ala Phe Phe Gly Leu Cys Gly Leu Ile Tyr Pro Ile Val Gln Tyr Asp			
275	280	285	
acc ttc ctc agc aac gaa tac cgc acc ggc atc agc tgg tcg ttc ggc			912
Thr Phe Leu Ser Asn Glu Tyr Arg Thr Gly Ile Ser Trp Ser Phe Gly			
290	295	300	
atg ctc ttt ttc ata tgg gcc atg ttt acg acg tgt cgc gcc gtc cgc			960
Met Leu Phe Phe Ile Trp Ala Met Phe Thr Thr Cys Arg Ala Val Arg			
305	310	315	320
tac ttt cgc gga cgc ggt agc ggc agt gtc aag tac cag gcg ctg gcc			1008
Tyr Phe Arg Gly Arg Gly Ser Gly Ser Val Lys Tyr Gln Ala Leu Ala			
325	330	335	
aca gcc tcc ggc gaa gaa gtc gct gtg ctc agt cac cac gac agc ttg			1056
Thr Ala Ser Gly Glu Glu Val Ala Val Leu Ser His His Asp Ser Leu			
340	345	350	
gaa agc cgt cgc ctc cgc gaa gaa gag gac gac gac gat gat gaa gac			1104
Glu Ser Arg Arg Leu Arg Glu Glu Glu Asp Asp Asp Asp Asp Glu Asp			
355	360	365	
ttc gag gac gct taa			1119
Phe Glu Asp Ala			
370			

<210> 4

<211> 372

<212> PRT

<213> Human cytomegalovirus

<400> 4

Met Ala Pro Ser His Val Asp Lys Val Asn Thr Arg Thr Trp Ser Ala			
1	5	10	15
Ser Ile Val Phe Met Val Leu Thr Phe Val Asn Val Ser Val His Leu			
20	25	30	
Val Leu Ser Asn Phe Pro His Leu Gly Tyr Pro Cys Val Tyr Tyr His			
35	40	45	
Val Val Asp Phe Glu Arg Leu Asn Met Ser Ala Tyr Asn Val Met His			
50	55	60	
Leu His Thr Pro Met Leu Phe Leu Asp Ser Val Gln Leu Val Cys Tyr			
65	70	75	80
Ala Val Phe Met Gln Leu Val Phe Leu Ala Val Thr Ile Tyr Tyr Leu			
85	90	95	
Val Cys Trp Ile Lys Ile Ser Met Arg Lys Asp Lys Gly Met Ser Leu			
100	105	110	
Asn Gln Ser Thr Arg Asp Ile Ser Tyr Met Gly Asp Ser Leu Thr Ala			
115	120	125	
Phe Leu Phe Ile Leu Ser Met Asp Thr Phe Gln Leu Phe Thr Leu Thr			
130	135	140	
Met Ser Phe Arg Leu Pro Ser Met Ile Ala Phe Met Ala Ala Val His			
145	150	155	160

Phe Phe Cys Leu Thr Ile Phe Asn Val Ser Met Val Thr Gln Tyr Arg
 165 170 175
 Ser Tyr Lys Arg Ser Leu Phe Phe Phe Ser Arg Leu His Pro Lys Leu
 180 185 190
 Lys Gly Thr Val Gln Phe Arg Thr Leu Ile Val Asn Leu Val Glu Val
 195 200 205
 Ala Leu Gly Phe Asn Thr Thr Val Val Ala Met Ala Leu Cys Tyr Gly
 210 215 220
 Phe Gly Asn Asn Phe Phe Val Arg Thr Gly His Met Val Leu Ala Val
 225 230 235 240
 Phe Val Val Tyr Ala Ile Ile Ser Ile Ile Tyr Phe Leu Leu Ile Glu
 245 250 255
 Ala Val Phe Phe Gln Tyr Val Lys Val Gln Phe Gly Tyr His Leu Gly
 260 265 270
 Ala Phe Phe Gly Leu Cys Gly Leu Ile Tyr Pro Ile Val Gln Tyr Asp
 275 280 285
 Thr Phe Leu Ser Asn Glu Tyr Arg Thr Gly Ile Ser Trp Ser Phe Gly
 290 295 300
 Met Leu Phe Phe Ile Trp Ala Met Phe Thr Thr Cys Arg Ala Val Arg
 305 310 315 320
 Tyr Phe Arg Gly Arg Gly Ser Gly Ser Val Lys Tyr Gln Ala Leu Ala
 325 330 335
 Thr Ala Ser Gly Glu Glu Val Ala Val Leu Ser His His Asp Ser Leu
 340 345 350
 Glu Ser Arg Arg Leu Arg Glu Glu Glu Asp Asp Asp Asp Asp Glu Asp
 355 360 365
 Phe Glu Asp Ala
 370

<210> 5

<211> 417

<212> DNA

<213> Human cytomegalovirus

<220>

<221> CDS

<222> (1)...(414)

<400> 5

atg gag tgg aac aca cta gta tta ggt ctt tta gtt tta tcg gta gtg 48
 Met Glu Trp Asn Thr Leu Val Leu Gly Leu Leu Val Leu Ser Val Val
 1 5 10 15

gca gag agt tct ggt aac aat tca tcc acg tca acc tct gca act aca 96
 Ala Glu Ser Ser Gly Asn Asn Ser Ser Thr Ser Thr Ser Ala Thr Thr
 20 25 30

tca aag tct tct gct agc gta tca act acc aaa cta aca aca gtt gca 144
 Ser Lys Ser Ser Ala Ser Val Ser Thr Thr Lys Leu Thr Thr Val Ala
 35 40 45

aca act tct gca aca act acg acg act acg acc tta tcg aca act agc 192
 Thr Thr Ser Ala Thr Thr Thr Thr Thr Thr Thr Thr Leu Ser Thr Thr Ser
 50 55 60

act aaa ctc agt tct acc acc cac gat cct aat gtg atg aga cga cat 240
 Thr Lys Leu Ser Ser Thr Thr His Asp Pro Asn Val Met Arg Arg His

65	70	75	80	
gcg aac gat gat ttt tac aag gcg cat tgc aca tcg cat atg tat gag				288
Ala Asn Asp Asp Phe Tyr Lys Ala His Cys Thr Ser His Met Tyr Glu				
	85	90	95	
ctc tca ctg tcc agc ttt gcg gcc tgg tgg act atg ctt aat gct cta				336
Leu Ser Leu Ser Ser Phe Ala Ala Trp Trp Thr Met Leu Asn Ala Leu				
	100	105	110	
att ctc atg gga gct ttt tgt att gta cta cga cat tgc tgc ttc cag				384
Ile Leu Met Gly Ala Phe Cys Ile Val Leu Arg His Cys Cys Phe Gln				
	115	120	125	
aac ttt act gca acc acc acc aaa ggc tat tga				417
Asn Phe Thr Ala Thr Thr Thr Lys Gly Tyr				
	130	135		

<210> 6
 <211> 138
 <212> PRT
 <213> Human cytomegalovirus

<400> 6
 Met Glu Trp Asn Thr Leu Val Leu Gly Leu Leu Val Leu Ser Val Val
 1 5 10 15
 Ala Glu Ser Ser Gly Asn Asn Ser Ser Thr Ser Thr Ser Ala Thr Thr
 20 25 30
 Ser Lys Ser Ser Ala Ser Val Ser Thr Thr Lys Leu Thr Thr Val Ala
 35 40 45
 Thr Thr Ser Ala Thr Thr Thr Thr Thr Thr Thr Leu Ser Thr Thr Ser
 50 55 60
 Thr Lys Leu Ser Ser Thr Thr His Asp Pro Asn Val Met Arg Arg His
 65 70 75 80
 Ala Asn Asp Asp Phe Tyr Lys Ala His Cys Thr Ser His Met Tyr Glu
 85 90 95
 Leu Ser Leu Ser Ser Phe Ala Ala Trp Trp Thr Met Leu Asn Ala Leu
 100 105 110
 Ile Leu Met Gly Ala Phe Cys Ile Val Leu Arg His Cys Cys Phe Gln
 115 120 125
 Asn Phe Thr Ala Thr Thr Thr Lys Gly Tyr
 130 135

<210> 7
 <211> 2232
 <212> DNA
 <213> Human cytomegalovirus

<220>
 <221> CDS
 <222> (1)...(2229)

65	70	75	80	
atg cgg ccc ggc ctc ccc ccc tac ctc act gtc ttc acc gtc tac ctc				48
Met Arg Pro Gly Leu Pro Pro Tyr Leu Thr Val Phe Thr Val Tyr Leu				
	5	10	15	

ctc agt cac cta cct tcg caa cga tat ggc gcg gac gcc gca tcc gaa Leu Ser His Leu Pro Ser Gln Arg Tyr Gly Ala Asp Ala Ala Ser Glu 20 25 30	96
gcg ctg gac cct cac gca ttt cac cta cta ctc aac acc tac ggg aga Ala Leu Asp Pro His Ala Phe His Leu Leu Leu Asn Thr Tyr Gly Arg 35 40 45	144
ccc atc cgc ttc ctg cgt gaa aac acc acc cag tgc acc tac aac agc Pro Ile Arg Phe Leu Arg Glu Asn Thr Thr Gln Cys Thr Tyr Asn Ser 50 55 60	192
agc ctc cgt aac agc acg gtc gtc agg gaa aac gcc atc agt ttc aac Ser Leu Arg Asn Ser Thr Val Val Arg Glu Asn Ala Ile Ser Phe Asn 65 70 75 80	240
ttt ttc caa agc tat aat caa tac tat gta ttc cat atg cct cga tgt Phe Phe Gln Ser Tyr Asn Gln Tyr Tyr Val Phe His Met Pro Arg Cys 85 90 95	288
ctt ttt gcg ggt cct ctg gcg gag cag ttt ctg aac cag gta gat ctg Leu Phe Ala Gly Pro Leu Ala Glu Gln Phe Leu Asn Gln Val Asp Leu 100 105 110	336
acc gaa acc cta gaa aga tac caa cag aga ctt aac acc tac gca ttg Thr Glu Thr Leu Glu Arg Tyr Gln Gln Arg Leu Asn Thr Tyr Ala Leu 115 120 125	384
gta tcc aaa gac ctg gcc agc tac cga tct ttt tcg cag cag ctg aag Val Ser Lys Asp Leu Ala Ser Tyr Arg Ser Phe Ser Gln Gln Leu Lys 130 135 140	432
gca caa gac agc ctg ggt cag cag ccc acc acc gtg cca ccg ccc att Ala Gln Asp Ser Leu Gly Gln Gln Pro Thr Thr Val Pro Pro Pro Ile 145 150 155 160	480
gat ctg tca ata cct cac gtt tgg atg cca ccc caa acc act cca cac Asp Leu Ser Ile Pro His Val Trp Met Pro Pro Gln Thr Thr Pro His 165 170 175	528
gac tgg aag gga tcg cac acc acc tcg gga cta cat cgg cca cac ttt Asp Trp Lys Gly Ser His Thr Thr Ser Gly Leu His Arg Pro His Phe 180 185 190	576
aac cag acc tgt atc ctc ttt gat gga cac gat ctg ctt ttc agc acc Asn Gln Thr Cys Ile Leu Phe Asp Gly His Asp Leu Leu Phe Ser Thr 195 200 205	624
gtt acg ccc tgt ctg cac cag ggc ttt tac ctc atg gac gaa cta cgt Val Thr Pro Cys Leu His Gln Gly Phe Tyr Leu Met Asp Glu Leu Arg 210 215 220	672
tac gtt aaa atc aca ctg acc gag gac ttc ttc gta gtt acg gta tct Tyr Val Lys Ile Thr Leu Thr Glu Asp Phe Phe Val Val Thr Val Ser 225 230 235 240	720

ata gac gac gac aca ccc atg ctg ctt atc ttc ggt cat ctt cca cgc Ile Asp Asp Asp Thr Pro Met Leu Leu Ile Phe Gly His Leu Pro Arg 245 250 255	768
gta ctc ttc aaa gcg ccc tat caa cgc gac aac ttt ata cta cga caa Val Leu Phe Lys Ala Pro Tyr Gln Arg Asp Asn Phe Ile Leu Arg Gln 260 265 270	816
act gaa aaa cac gag ctc ctg gta cta gtt aag aaa gct caa cta aac Thr Glu Lys His Glu Leu Leu Val Lys Lys Ala Gln Leu Asn 275 280 285	864
cgt cac tcc tat ctc aaa gac tcg gac ttt ctc gac gcc gca ctc gac Arg His Ser Tyr Leu Lys Asp Ser Asp Phe Leu Asp Ala Ala Leu Asp 290 295 300	912
ttc aac tac ctg gac ctc agc gca ctg tta cgt aac agc ttt cac cgt Phe Asn Tyr Leu Asp Leu Ser Ala Leu Leu Arg Asn Ser Phe His Arg 305 310 315 320	960
tac gct gta gac gta ctc aaa agc ggt cga tgt caa atg ttg gac cgc Tyr Ala Val Asp Val Leu Lys Ser Gly Arg Cys Gln Met Leu Asp Arg 325 330 335	1008
cgc acg gta gaa atg gcc ttc gcc tac gca tta gca ctg ttc gcg gca Arg Thr Val Glu Met Ala Phe Ala Tyr Ala Leu Ala Leu Phe Ala Ala 340 345 350	1056
gcc cga caa gaa gag gcc ggc acc gaa atc tcc atc cca cga gcc cta Ala Arg Gln Glu Glu Ala Gly Thr Glu Ile Ser Ile Pro Arg Ala Leu 355 360 365	1104
gac cgc cag gcc gca ctc tta caa ata caa gaa ttt atg atc acc tgc Asp Arg Gln Ala Ala Leu Leu Gln Ile Gln Glu Phe Met Ile Thr Cys 370 375 380	1152
ctc tca caa aca cca cca cgc acc aca ttg ctg cta tat ccc aca gcc Leu Ser Gln Thr Pro Pro Arg Thr Thr Leu Leu Leu Tyr Pro Thr Ala 385 390 395 400	1200
gtg gac ctg gcc aaa cga gcc ctc tgg acg ccg gac cag atc acc gac Val Asp Leu Ala Lys Arg Ala Leu Trp Thr Pro Asp Gln Ile Thr Asp 405 410 415	1248
atc acc agc ctc gta cgc ctg gtc tac ata ctt tct aaa cag aat cag Ile Thr Ser Leu Val Arg Leu Val Tyr Ile Leu Ser Lys Gln Asn Gln 420 425 430	1296
caa cat ctc att ccc cag tgg gca cta cga cag atc gcc gac ttt gcc Gln His Leu Ile Pro Gln Trp Ala Leu Arg Gln Ile Ala Asp Phe Ala 435 440 445	1344
cta caa tta cac aaa acg cac ctg gcc tct ttt ctt tca gcc ttc gcg Leu Gln Leu His Lys Thr His Leu Ala Ser Phe Leu Ser Ala Phe Ala 450 455 460	1392
cgc caa gaa ctc tac ctc atg ggc agc ctc gtc cac tcc atg ttg gta	1440

Arg Gln Glu Leu Tyr Leu Met Gly Ser Leu Val His Ser Met Leu Val	
465 470 475 480	
cat acg acg gag aga cgc gaa atc ttc atc gta gaa acg ggc ctc tgt	1488
His Thr Thr Glu Arg Arg Glu Ile Phe Ile Val Glu Thr Gly Leu Cys	
485 490 495	
tca ttg gcc gag cta tca cac ttt acg cag ttg cta gct cat ccg cac	1536
Ser Leu Ala Glu Leu Ser His Phe Thr Gln Leu Leu Ala His Pro His	
500 505 510	
cac gaa tac ctc agc gac ctg tac aca ccc tgt tcc agt agc ggg cga	1584
His Glu Tyr Leu Ser Asp Leu Tyr Thr Pro Cys Ser Ser Ser Gly Arg	
515 520 525	
cgc gat cac tcg ctc gaa cgc ctc acg cgt ctc ttc ccc gat gcc acc	1632
Arg Asp His Ser Leu Glu Arg Leu Thr Arg Leu Phe Pro Asp Ala Thr	
530 535 540	
gtt cct gct acc gtt ccc gcc gcc ctc tcc atc cta tct acc atg caa	1680
Val Pro Ala Thr Val Pro Ala Ala Leu Ser Ile Leu Ser Thr Met Gln	
545 550 555 560	
cca agc acg ctg gaa acc ttc ccc gac ctg ttt tgt ctg ccg ctc ggc	1728
Pro Ser Thr Leu Glu Thr Phe Pro Asp Leu Phe Cys Leu Pro Leu Gly	
565 570 575	
gaa tcc ttc tcc gcg cta acc gtc tcc gaa cac gtc agt tat gtc gta	1776
Glu Ser Phe Ser Ala Leu Thr Val Ser Glu His Val Ser Tyr Val Val	
580 585 590	
aca aac cag tac ctg atc aaa ggt atc tcc tac cct gtc tcc acc acc	1824
Thr Asn Gln Tyr Leu Ile Lys Gly Ile Ser Tyr Pro Val Ser Thr Thr	
595 600 605	
gtc gta ggc cag agc ctc atc atc acc caa acg gac agt caa act aaa	1872
Val Val Gly Gln Ser Leu Ile Ile Thr Gln Thr Asp Ser Gln Thr Lys	
610 615 620	
tgc gaa cta acg cgc aac atg cac acc aca cac agc atc aca gcg gcg	1920
Cys Glu Leu Thr Arg Asn Met His Thr Thr His Ser Ile Thr Ala Ala	
625 630 635 640	
ctc aac att tca cta gaa aac tgc gcc ttt tgc caa agc gcc ctg cta	1968
Leu Asn Ile Ser Leu Glu Asn Cys Ala Phe Cys Gln Ser Ala Leu Leu	
645 650 655	
gaa tac gac gac acg caa ggc gtc atc aac atc atg tac atg cac gac	2016
Glu Tyr Asp Asp Thr Gln Gly Val Ile Asn Ile Met Tyr Met His Asp	
660 665 670	
tcg gac gac gtc ctt ttc gcc ctg gat ccc tac aac gaa gtg gtg gtc	2064
Ser Asp Asp Val Leu Phe Ala Leu Asp Pro Tyr Asn Glu Val Val Val	
675 680 685	
tca tct ccg cga act cac tac ctc atg ctt ttg aaa aac ggt acg gtc	2112
Ser Ser Pro Arg Thr His Tyr Leu Met Leu Leu Lys Asn Gly Thr Val	

690	695	700	
cta gaa gta act gac gtc gtc gtg gac gcc acc gac agt cgt ctc ctc			2160
Leu Glu Val Thr Asp Val Val Val Asp Ala Thr Asp Ser Arg Leu Leu			
705	710	715	720
atg atg tcc gtc tac gcg cta tcg gcc atc atc ggc atc tat ctg ctc			2208
Met Met Ser Val Tyr Ala Leu Ser Ala Ile Ile Gly Ile Tyr Leu Leu			
	725	730	735
tac cgc atg ctc aag aca tgc tga			2232
Tyr Arg Met Leu Lys Thr Cys			
740			

<210> 8

<211> 743

<212> PRT

<213> Human cytomegalovirus

<400> 8

Met Arg Pro Gly Leu Pro Pro Tyr Leu Thr Val Phe Thr Val Tyr Leu			
1	5	10	15
Leu Ser His Leu Pro Ser Gln Arg Tyr Gly Ala Asp Ala Ala Ser Glu			
20	25	30	
Ala Leu Asp Pro His Ala Phe His Leu Leu Leu Asn Thr Tyr Gly Arg			
35	40	45	
Pro Ile Arg Phe Leu Arg Glu Asn Thr Thr Gln Cys Thr Tyr Asn Ser			
50	55	60	
Ser Leu Arg Asn Ser Thr Val Val Arg Glu Asn Ala Ile Ser Phe Asn			
65	70	75	80
Phe Phe Gln Ser Tyr Asn Gln Tyr Tyr Val Phe His Met Pro Arg Cys			
85	90	95	
Leu Phe Ala Gly Pro Leu Ala Glu Gln Phe Leu Asn Gln Val Asp Leu			
100	105	110	
Thr Glu Thr Leu Glu Arg Tyr Gln Gln Arg Leu Asn Thr Tyr Ala Leu			
115	120	125	
Val Ser Lys Asp Leu Ala Ser Tyr Arg Ser Phe Ser Gln Gln Leu Lys			
130	135	140	
Ala Gln Asp Ser Leu Gly Gln Gln Pro Thr Thr Val Pro Pro Pro Ile			
145	150	155	160
Asp Leu Ser Ile Pro His Val Trp Met Pro Pro Gln Thr Thr Pro His			
165	170	175	
Asp Trp Lys Gly Ser His Thr Thr Ser Gly Leu His Arg Pro His Phe			
180	185	190	
Asn Gln Thr Cys Ile Leu Phe Asp Gly His Asp Leu Leu Phe Ser Thr			
195	200	205	
Val Thr Pro Cys Leu His Gln Gly Phe Tyr Leu Met Asp Glu Leu Arg			
210	215	220	
Tyr Val Lys Ile Thr Leu Thr Glu Asp Phe Phe Val Val Thr Val Ser			
225	230	235	240
Ile Asp Asp Asp Thr Pro Met Leu Leu Ile Phe Gly His Leu Pro Arg			
245	250	255	
Val Leu Phe Lys Ala Pro Tyr Gln Arg Asp Asn Phe Ile Leu Arg Gln			
260	265	270	
Thr Glu Lys His Glu Leu Leu Val Leu Val Lys Lys Ala Gln Leu Asn			
275	280	285	

740

<210> 9
 <211> 921
 <212> DNA
 <213> Human cytomegalovirus

<220>
 <221> CDS
 <222> (1)...(918)

<400> 9
 cgt ttt agg gat cga aga cct gag cgc caa ctt tcg gcg cca act ggc 48
 Arg Phe Arg Asp Arg Arg Pro Glu Arg Gln Leu Ser Ala Pro Thr Gly
 1 5 10 15
 tcc tta ccg tca cac tct cat cgt gcc gca gac ttg atg tgc cgc cgc 96
 Ser Leu Pro Ser His Ser His Arg Ala Ala Asp Leu Met Cys Arg Arg
 20 25 30
 ccg gat tgc ggc ttc tct ttc tca cct gga ccg gtg gta ctg ctg tgg 144
 Pro Asp Cys Gly Phe Ser Phe Ser Pro Gly Pro Val Val Leu Leu Trp
 35 40 45
 tgt tgc ctt ctg ctg ccc att gtt tcc tca gtc gcc gtc agc gtc gct 192
 Cys Cys Leu Leu Leu Pro Ile Val Ser Ser Val Ala Val Ser Val Ala
 50 55 60
 cct acc gcc gcc gag aaa gtc ccc gcg gag tgc ccc gaa cta acg cgt 240
 Pro Thr Ala Ala Glu Lys Val Pro Ala Glu Cys Pro Glu Leu Thr Arg
 65 70 75 80
 cga tgc ctg ttg ggt gag gtg ttt cag ggt gac aag tat gaa agt tgg 288
 Arg Cys Leu Leu Gly Glu Val Phe Gln Gly Asp Lys Tyr Glu Ser Trp
 85 90 95
 ctg cgc ccg ttg gtg aat gtt acc aga cgc gat ggc ccg cta tcg caa 336
 Leu Arg Pro Leu Val Asn Val Thr Arg Arg Asp Gly Pro Leu Ser Gln
 100 105 110
 ctt att cgt tac cgt ccc gtt acg ccg gag gcc gcc aac tcc gtg ctg 384
 Leu Ile Arg Tyr Arg Pro Val Thr Pro Glu Ala Ala Asn Ser Val Leu
 115 120 125
 ttg gac gat gct ttc ctg gac act ctg gcc ctg ctg tac aac aat ccg 432
 Leu Asp Asp Ala Phe Leu Asp Thr Leu Ala Leu Leu Tyr Asn Asn Pro
 130 135 140
 gat caa ttg cgg gcc ctg ctg acg ctg ttg agc tcg gac aca gcg ccg 480
 Asp Gln Leu Arg Ala Leu Leu Thr Leu Leu Ser Ser Asp Thr Ala Pro
 145 150 155 160
 cgc tgg atg acg gtg atg cgc ggc tac agc gag tgc ggc gat ggc tcg 528
 Arg Trp Met Thr Val Met Arg Gly Tyr Ser Glu Cys Gly Asp Gly Ser
 165 170 175
 ccg gcc gtg tac acg tgc gtg gac gac ctg tgc cgc ggc tac gac ctc 576

Pro	Ala	Val	Tyr	Thr	Cys	Val	Asp	Asp	Leu	Cys	Arg	Gly	Tyr	Asp	Leu		
			180					185					190				
acg	cga	ctg	tca	tac	ggg	cgc	agc	atc	ttc	acg	gaa	cac	gtg	tta	ggc	624	
Thr	Arg	Leu	Ser	Tyr	Gly	Arg	Ser	Ile	Phe	Thr	Glu	His	Val	Leu	Gly		
		195					200				205						
ttc	gag	ctg	gtg	cca	ccg	tct	ctc	ttt	aac	gtg	gtg	gtg	gcc	ata	cgc	672	
Phe	Glu	Leu	Val	Pro	Pro	Ser	Leu	Phe	Asn	Val	Val	Val	Ala	Ile	Arg		
	210					215				220							
aac	gaa	gcc	acg	cgt	acc	aac	cgc	gcc	gtg	cgt	ctg	ccc	gtg	agc	acc	720	
Asn	Glu	Ala	Thr	Arg	Thr	Asn	Arg	Ala	Val	Arg	Leu	Pro	Val	Ser	Thr		
225					230				235						240		
gct	gcc	gcg	ccc	gag	ggc	atc	aca	ctc	ttt	tac	ggc	ctg	tac	aac	gca	768	
Ala	Ala	Ala	Pro	Glu	Gly	Ile	Thr	Leu	Phe	Tyr	Gly	Leu	Tyr	Asn	Ala		
			245					250						255			
gtg	aag	gaa	ttc	tgc	ctg	cgt	cac	cag	ctg	gac	ccg	ccg	cta	cta	cgc	816	
Val	Lys	Glu	Phe	Cys	Leu	Arg	His	Gln	Leu	Asp	Pro	Pro	Leu	Leu	Arg		
		260					265				270						
cac	cta	gat	aaa	tac	tac	gcc	gga	ctg	ccg	ccc	gag	ctg	aag	cag	acg	864	
His	Leu	Asp	Lys	Tyr	Tyr	Ala	Gly	Leu	Pro	Pro	Glu	Leu	Lys	Gln	Thr		
		275					280				285						
cgc	gtc	aac	ctg	ccg	gct	cac	tcg	cgc	tat	ggc	cct	caa	gca	gtg	gat	912	
Arg	Val	Asn	Leu	Pro	Ala	His	Ser	Arg	Tyr	Gly	Pro	Gln	Ala	Val	Asp		
	290					295				300							
gct	cgc	taa														921	
Ala	Arg																
305																	

<210> 10

<211> 306

<212> PRT

<213> Human cytomegalovirus

<400> 10

Arg	Phe	Arg	Asp	Arg	Arg	Pro	Glu	Arg	Gln	Leu	Ser	Ala	Pro	Thr	Gly		
1				5					10					15			
Ser	Leu	Pro	Ser	His	Ser	His	Arg	Ala	Ala	Asp	Leu	Met	Cys	Arg	Arg		
			20				25						30				
Pro	Asp	Cys	Gly	Phe	Ser	Phe	Ser	Pro	Gly	Pro	Val	Val	Leu	Leu	Trp		
		35					40					45					
Cys	Cys	Leu	Leu	Leu	Pro	Ile	Val	Ser	Ser	Val	Ala	Val	Ser	Val	Ala		
	50					55					60						
Pro	Thr	Ala	Ala	Glu	Lys	Val	Pro	Ala	Glu	Cys	Pro	Glu	Leu	Thr	Arg		
65					70				75					80			
Arg	Cys	Leu	Leu	Gly	Glu	Val	Phe	Gln	Gly	Asp	Lys	Tyr	Glu	Ser	Trp		
				85				90					95				
Leu	Arg	Pro	Leu	Val	Asn	Val	Thr	Arg	Arg	Asp	Gly	Pro	Leu	Ser	Gln		
		100						105				110					
Leu	Ile	Arg	Tyr	Arg	Pro	Val	Thr	Pro	Glu	Ala	Ala	Asn	Ser	Val	Leu		

115	120	125
Leu Asp Asp Ala Phe Leu Asp Thr Leu Ala Leu Leu Tyr Asn Asn Pro		
130	135	140
Asp Gln Leu Arg Ala Leu Leu Thr Leu Leu Ser Ser Asp Thr Ala Pro		
145	150	155
Arg Trp Met Thr Val Met Arg Gly Tyr Ser Glu Cys Gly Asp Gly Ser		
165	170	175
Pro Ala Val Tyr Thr Cys Val Asp Asp Leu Cys Arg Gly Tyr Asp Leu		
180	185	190
Thr Arg Leu Ser Tyr Gly Arg Ser Ile Phe Thr Glu His Val Leu Gly		
195	200	205
Phe Glu Leu Val Pro Pro Ser Leu Phe Asn Val Val Val Ala Ile Arg		
210	215	220
Asn Glu Ala Thr Arg Thr Asn Arg Ala Val Arg Leu Pro Val Ser Thr		
225	230	235
Ala Ala Ala Pro Glu Gly Ile Thr Leu Phe Tyr Gly Leu Tyr Asn Ala		
245	250	255
Val Lys Glu Phe Cys Leu Arg His Gln Leu Asp Pro Pro Leu Leu Arg		
260	265	270
His Leu Asp Lys Tyr Tyr Ala Gly Leu Pro Pro Glu Leu Lys Gln Thr		
275	280	285
Arg Val Asn Leu Pro Ala His Ser Arg Tyr Gly Pro Gln Ala Val Asp		
290	295	300
Ala Arg		
305		

<210> 11

<211> 1401

<212> DNA

<213> Human cytomegalovirus

<220>

<221> CDS

<222> (1)...(1398)

<400> 11

atg ggg aga aaa gag atg atg gtg aga gac gtc cct aag atg gtg ttt	48
Met Gly Arg Lys Glu Met Met Val Arg Asp Val Pro Lys Met Val Phe	
1 5 10 15	
cta ata tct ata tct ttc ttg ctt gtt tct ttc ata aac tgt aaa gtt	96
Leu Ile Ser Ile Ser Phe Leu Leu Val Ser Phe Ile Asn Cys Lys Val	
20 25 30	
atg tca aaa gcg ctt tat aat cgt cct tgg agg ggc ttg gta ctg tct	144
Met Ser Lys Ala Leu Tyr Asn Arg Pro Trp Arg Gly Leu Val Leu Ser	
35 40 45	
aag ata ggc aaa tat aaa tta gat cag ctt aag tta gaa att ttg aga	192
Lys Ile Gly Lys Tyr Lys Leu Asp Gln Leu Lys Leu Glu Ile Leu Arg	
50 55 60	
caa cta gaa acg act att tct aca aaa tac aat gta agt aaa caa ccg	240
Gln Leu Glu Thr Thr Ile Ser Thr Lys Tyr Asn Val Ser Lys Gln Pro	
65 70 75 80	
gtt aaa aat ctc act atg aac atg aca gag ttt cca caa tac tac att	288

Val	Lys	Asn	Leu	Thr	Met	Asn	Met	Thr	Glu	Phe	Pro	Gln	Tyr	Tyr	Ile	
				85					90						95	
tta	gcg	ggc	ccc	att	cag	aat	tat	agt	ata	acc	tat	ctg	tgg	ttt	gat	336
Leu	Ala	Gly	Pro	Ile	Gln	Asn	Tyr	Ser	Ile	Thr	Tyr	Leu	Trp	Phe	Asp	
			100					105					110			
ttt	tat	agt	acc	cag	ctt	aga	aaa	ccc	gca	aaa	tac	gtt	tac	tca	cag	384
Phe	Tyr	Ser	Thr	Gln	Leu	Arg	Lys	Pro	Ala	Lys	Tyr	Val	Tyr	Ser	Gln	
		115					120					125				
tac	aat	cat	acg	gct	aaa	acg	ata	aca	ttc	aga	ccc	cca	cct	tgt	ggc	432
Tyr	Asn	His	Thr	Ala	Lys	Thr	Ile	Thr	Phe	Arg	Pro	Pro	Pro	Cys	Gly	
	130					135					140					
act	gtg	cct	tcc	atg	act	tgt	ctt	tcc	gaa	atg	cta	aac	gtt	tcc	aaa	480
Thr	Val	Pro	Ser	Met	Thr	Cys	Leu	Ser	Glu	Met	Leu	Asn	Val	Ser	Lys	
145					150				155						160	
cgt	aat	gat	act	ggc	gaa	caa	ggc	tgc	ggc	aat	ttc	acc	acg	ttc	aac	528
Arg	Asn	Asp	Thr	Gly	Glu	Gln	Gly	Cys	Gly	Asn	Phe	Thr	Thr	Phe	Asn	
			165					170						175		
ccc	atg	ttt	ttc	aat	gta	ccg	cgt	tgg	aac	acc	aaa	ttg	tac	gtg	ggc	576
Pro	Met	Phe	Phe	Asn	Val	Pro	Arg	Trp	Asn	Thr	Lys	Leu	Tyr	Val	Gly	
			180					185					190			
ccg	act	aag	gtt	aac	gta	gat	agt	caa	acg	att	tat	ttt	cta	ggc	tta	624
Pro	Thr	Lys	Val	Asn	Val	Asp	Ser	Gln	Thr	Ile	Tyr	Phe	Leu	Gly	Leu	
		195					200					205				
acc	gcc	ctg	ctt	tta	cgt	tac	gca	caa	cgc	aac	tgt	aca	cac	agt	ttc	672
Thr	Ala	Leu	Leu	Leu	Arg	Tyr	Ala	Gln	Arg	Asn	Cys	Thr	His	Ser	Phe	
	210					215					220					
tac	ctg	gtt	aac	gcc	atg	agc	cgg	aat	cta	ttt	cgc	gtc	ccc	aag	tat	720
Tyr	Leu	Val	Asn	Ala	Met	Ser	Arg	Asn	Leu	Phe	Arg	Val	Pro	Lys	Tyr	
225					230				235						240	
att	aac	ggc	acc	aag	tta	aaa	aac	act	atg	cga	aaa	cta	aaa	cgt	aaa	768
Ile	Asn	Gly	Thr	Lys	Leu	Lys	Asn	Thr	Met	Arg	Lys	Leu	Lys	Arg	Lys	
			245					250						255		
caa	gcg	ccc	gtt	aag	gaa	caa	ttc	gaa	aaa	aaa	gct	aag	aaa	act	cag	816
Gln	Ala	Pro	Val	Lys	Glu	Gln	Phe	Glu	Lys	Lys	Ala	Lys	Lys	Thr	Gln	
			260					265						270		
agt	act	act	acg	cca	tac	ttt	tcc	tat	aca	acg	tct	gcc	gct	ctc	aac	864
Ser	Thr	Thr	Thr	Pro	Tyr	Phe	Ser	Tyr	Thr	Thr	Ser	Ala	Ala	Leu	Asn	
		275					280					285				
gtc	act	act	aac	gtg	act	tat	agt	att	act	acc	gcc	gca	agg	cgg	gtt	912
Val	Thr	Thr	Asn	Val	Thr	Tyr	Ser	Ile	Thr	Thr	Ala	Ala	Arg	Arg	Val	
	290					295					300					
tcc	acg	tct	aca	att	gct	tat	cgt	cct	gat	agc	agc	ttt	atg	aag	tcc	960
Ser	Thr	Ser	Thr	Ile	Ala	Tyr	Arg	Pro	Asp	Ser	Ser	Phe	Met	Lys	Ser	

305	310	315	320	
att atg gcc aca cag tta agg gac cta gca acg tgg gtg tat acc act				1008
Ile Met Ala Thr Gln Leu Arg Asp Leu Ala Thr Trp Val Tyr Thr Thr	325	330	335	
cta cgt tac cgg caa aat cct ttt tgt gaa cca agc cgc aac cga acc				1056
Leu Arg Tyr Arg Gln Asn Pro Phe Cys Glu Pro Ser Arg Asn Arg Thr	340	345	350	
gcc gtg tca gaa ttt atg aaa aac acg cac gta cta atc cgt aac gaa				1104
Ala Val Ser Glu Phe Met Lys Asn Thr His Val Leu Ile Arg Asn Glu	355	360	365	
acg ccg tac act att tac ggt act ctc gac atg agc tcc tta tat tac				1152
Thr Pro Tyr Thr Ile Tyr Gly Thr Leu Asp Met Ser Ser Leu Tyr Tyr	370	375	380	
aac gaa acc atg ttc gtg gaa aac aaa aca gct tcc gat agt aac aaa				1200
Asn Glu Thr Met Phe Val Glu Asn Lys Thr Ala Ser Asp Ser Asn Lys	385	390	395	400
act aca cct acg tca cca tca atg ggg ttt cag aga aca ttt ata gat				1248
Thr Thr Pro Thr Ser Pro Ser Met Gly Phe Gln Arg Thr Phe Ile Asp	405	410	415	
ccc ctg tgg gac tat cta gac tcg ctg ctg ttt cta gat gag att cgt				1296
Pro Leu Trp Asp Tyr Leu Asp Ser Leu Leu Phe Leu Asp Glu Ile Arg	420	425	430	
aac ttt agc ctc cgg tca ccc acg tat gta aac ctt acc ccg ccg gaa				1344
Asn Phe Ser Leu Arg Ser Pro Thr Tyr Val Asn Leu Thr Pro Pro Glu	435	440	445	
cac cgc cgg gct gta aat ctg tcc acc ctc aat agc ctt tgg tgg tgg				1392
His Arg Arg Ala Val Asn Leu Ser Thr Leu Asn Ser Leu Trp Trp Trp	450	455	460	
ttg cag taa				1401
Leu Gln				
465				

<210> 12

<211> 466

<212> PRT

<213> Human cytomegalovirus

<400> 12

Met Gly Arg Lys Glu Met Met Val Arg Asp Val Pro Lys Met Val Phe				
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Leu Ile Ser Ile Ser Phe Leu Leu Val Ser Phe Ile Asn Cys Lys Val				
20	25	30		
Met Ser Lys Ala Leu Tyr Asn Arg Pro Trp Arg Gly Leu Val Leu Ser				
35	40	45		
Lys Ile Gly Lys Tyr Lys Leu Asp Gln Leu Lys Leu Glu Ile Leu Arg				
50	55	60		

Gln Leu Glu Thr Thr Ile Ser Thr Lys Tyr Asn Val Ser Lys Gln Pro
 65 70 75 80
 Val Lys Asn Leu Thr Met Asn Met Thr Glu Phe Pro Gln Tyr Tyr Ile
 85 90 95
 Leu Ala Gly Pro Ile Gln Asn Tyr Ser Ile Thr Tyr Leu Trp Phe Asp
 100 105 110
 Phe Tyr Ser Thr Gln Leu Arg Lys Pro Ala Lys Tyr Val Tyr Ser Gln
 115 120 125
 Tyr Asn His Thr Ala Lys Thr Ile Thr Phe Arg Pro Pro Pro Cys Gly
 130 135 140
 Thr Val Pro Ser Met Thr Cys Leu Ser Glu Met Leu Asn Val Ser Lys
 145 150 155 160
 Arg Asn Asp Thr Gly Glu Gln Gly Cys Gly Asn Phe Thr Thr Phe Asn
 165 170 175
 Pro Met Phe Phe Asn Val Pro Arg Trp Asn Thr Lys Leu Tyr Val Gly
 180 185 190
 Pro Thr Lys Val Asn Val Asp Ser Gln Thr Ile Tyr Phe Leu Gly Leu
 195 200 205
 Thr Ala Leu Leu Leu Arg Tyr Ala Gln Arg Asn Cys Thr His Ser Phe
 210 215 220
 Tyr Leu Val Asn Ala Met Ser Arg Asn Leu Phe Arg Val Pro Lys Tyr
 225 230 235 240
 Ile Asn Gly Thr Lys Leu Lys Asn Thr Met Arg Lys Leu Lys Arg Lys
 245 250 255
 Gln Ala Pro Val Lys Glu Gln Phe Glu Lys Lys Ala Lys Lys Thr Gln
 260 265 270
 Ser Thr Thr Thr Pro Tyr Phe Ser Tyr Thr Thr Ser Ala Ala Leu Asn
 275 280 285
 Val Thr Thr Asn Val Thr Tyr Ser Ile Thr Thr Ala Ala Arg Arg Val
 290 295 300
 Ser Thr Ser Thr Ile Ala Tyr Arg Pro Asp Ser Ser Phe Met Lys Ser
 305 310 315 320
 Ile Met Ala Thr Gln Leu Arg Asp Leu Ala Thr Trp Val Tyr Thr Thr
 325 330 335
 Leu Arg Tyr Arg Gln Asn Pro Phe Cys Glu Pro Ser Arg Asn Arg Thr
 340 345 350
 Ala Val Ser Glu Phe Met Lys Asn Thr His Val Leu Ile Arg Asn Glu
 355 360 365
 Thr Pro Tyr Thr Ile Tyr Gly Thr Leu Asp Met Ser Ser Leu Tyr Tyr
 370 375 380
 Asn Glu Thr Met Phe Val Glu Asn Lys Thr Ala Ser Asp Ser Asn Lys
 385 390 395 400
 Thr Thr Pro Thr Ser Pro Ser Met Gly Phe Gln Arg Thr Phe Ile Asp
 405 410 415
 Pro Leu Trp Asp Tyr Leu Asp Ser Leu Leu Phe Leu Asp Glu Ile Arg
 420 425 430
 Asn Phe Ser Leu Arg Ser Pro Thr Tyr Val Asn Leu Thr Pro Pro Glu
 435 440 445
 His Arg Arg Ala Val Asn Leu Ser Thr Leu Asn Ser Leu Trp Trp Trp
 450 455 460
 Leu Gln
 465

<210> 13

<211> 1686

<212> DNA

<213> Human cytomegalovirus

<220>

<221> CDS

<222> (1)...(1683)

<400> 13

atg	gag	tcg	cgc	ggt	cgc	cgt	tgt	ccc	gaa	atg	ata	tcc	gta	ctg	ggt	48
Met	Glu	Ser	Arg	Gly	Arg	Arg	Cys	Pro	Glu	Met	Ile	Ser	Val	Leu	Gly	
1				5				10						15		

ccc	att	tcg	ggg	cac	gtg	ctg	aaa	gcc	gtg	ttt	agt	cgc	ggc	gat	acg	96
Pro	Ile	Ser	Gly	His	Val	Leu	Lys	Ala	Val	Phe	Ser	Arg	Gly	Asp	Thr	
			20					25					30			

cgc	gtg	ctg	cgc	cac	gag	acg	cga	ctc	ctg	cag	acg	ggt	atc	cac	gta	144
Pro	Val	Leu	Pro	His	Glu	Thr	Arg	Leu	Leu	Gln	Thr	Gly	Ile	His	Val	
		35					40					45				

cgc	gtg	agc	cag	ccc	tcg	ctg	atc	ttg	gta	tcg	cag	tac	acg	ccc	gac	192
Arg	Val	Ser	Gln	Pro	Ser	Leu	Ile	Leu	Val	Ser	Gln	Tyr	Thr	Pro	Asp	
	50					55				60						

tcg	acg	cca	tgc	cac	cgc	ggc	gac	aat	cag	ctg	cag	gtg	cag	cac	acg	240
Ser	Thr	Pro	Cys	His	Arg	Gly	Asp	Asn	Gln	Leu	Gln	Val	Gln	His	Thr	
	65				70				75					80		

tac	ttt	acg	ggc	agc	gag	gtg	gag	aac	gtg	tcg	gtc	aac	gtg	cac	aac	288
Tyr	Phe	Thr	Gly	Ser	Glu	Val	Glu	Asn	Val	Ser	Val	Asn	Val	His	Asn	
			85					90						95		

ccc	acg	ggc	cga	agc	atc	tgc	ccc	agc	cag	gag	ccc	atg	tcg	atc	tat	336
Pro	Thr	Gly	Arg	Ser	Ile	Cys	Pro	Ser	Gln	Glu	Pro	Met	Ser	Ile	Tyr	
		100					105					110				

gtg	tac	gcg	ctg	ccg	ctc	aag	atg	ctg	aac	atc	ccc	agc	atc	aac	gtg	384
Val	Tyr	Ala	Leu	Pro	Leu	Lys	Met	Leu	Asn	Ile	Pro	Ser	Ile	Asn	Val	
		115					120					125				

cac	cac	tac	ccg	tcg	gcg	gcc	gag	cgc	aaa	cac	cga	cac	ctg	ccc	gta	432
His	His	Tyr	Pro	Ser	Ala	Ala	Glu	Arg	Lys	His	Arg	His	Leu	Pro	Val	
		130				135					140					

gct	gac	gct	gtg	att	cac	gcg	tcg	ggc	aag	cag	atg	tgg	cag	gcg	cgt	480
Ala	Asp	Ala	Val	Ile	His	Ala	Ser	Gly	Lys	Gln	Met	Trp	Gln	Ala	Arg	
145					150				155					160		

ctc	acg	gtc	tcg	gga	ctg	gcc	tgg	acg	cgt	cag	cag	aac	cag	tgg	aaa	528
Leu	Thr	Val	Ser	Gly	Leu	Ala	Trp	Thr	Arg	Gln	Gln	Asn	Gln	Trp	Lys	
				165					170					175		

gag	ccc	gac	gtc	tac	tac	acg	tca	gcg	ttc	gtg	ttt	ccc	acc	aag	gac	576
Glu	Pro	Asp	Val	Tyr	Tyr	Thr	Ser	Ala	Phe	Val	Phe	Pro	Thr	Lys	Asp	
			180					185					190			

gtg	gca	ctg	cgg	cac	gtg	gtg	tgc	gcg	cac	gag	ctg	gtt	tgc	tcc	atg	624
Val	Ala	Leu	Arg	His	Val	Val	Cys	Ala	His	Glu	Leu	Val	Cys	Ser	Met	
		195					200						205			

gag aac acg cgc gca acc aag atg cag gtg ata ggt gac cag tac gtc Glu Asn Thr Arg Ala Thr Lys Met Gln Val Ile Gly Asp Gln Tyr Val 210 215 220	672
aag gtg tac ctg gag tcc ttc tgc gag gac gtg ccc tcc ggc aag ctc Lys Val Tyr Leu Glu Ser Phe Cys Glu Asp Val Pro Ser Gly Lys Leu 225 230 235 240	720
ttt atg cac gtc acg ctg ggc tct gac gtg gaa gag gac ctg acg atg Phe Met His Val Thr Leu Gly Ser Asp Val Glu Glu Asp Leu Thr Met 245 250 255	768
acc cgc aac ccg caa ccc ttc atg cgc ccc cac gag cgc aac ggc ttt Thr Arg Asn Pro Gln Pro Phe Met Arg Pro His Glu Arg Asn Gly Phe 260 265 270	816
acg gtg ttg tgt ccc aaa aat atg ata atc aaa ccg ggc aag atc tcg Thr Val Leu Cys Pro Lys Asn Met Ile Ile Lys Pro Gly Lys Ile Ser 275 280 285	864
cac atc atg ctg gat gtg gct ttt acc tca cac gag cat ttt ggg ctg His Ile Met Leu Asp Val Ala Phe Thr Ser His Glu His Phe Gly Leu 290 295 300	912
ctg tgt ccc aag agc atc ccg ggc ctg agc atc tca ggt aac ctg ttg Leu Cys Pro Lys Ser Ile Pro Gly Leu Ser Ile Ser Gly Asn Leu Leu 305 310 315 320	960
atg aac ggg cag cag atc ttc ctg gag gta caa gcc ata cgc gag acc Met Asn Gly Gln Gln Ile Phe Leu Glu Val Gln Ala Ile Arg Glu Thr 325 330 335	1008
gtg gaa ctg cgt cag tac gat ccc gtg gct gcg ctc ttc ttt ttc gat Val Glu Leu Arg Gln Tyr Asp Pro Val Ala Ala Leu Phe Phe Phe Asp 340 345 350	1056
atc gac ttg ctg ctg cag cgc ggg oct cag tac agc gag cac ccc acc Ile Asp Leu Leu Leu Gln Arg Gly Pro Gln Tyr Ser Glu His Pro Thr 355 360 365	1104
ttc acc agc cag tat cgc atc cag ggc aag ctt gag tac cga cac acc Phe Thr Ser Gln Tyr Arg Ile Gln Gly Lys Leu Glu Tyr Arg His Thr 370 375 380	1152
tgg gac cgg cac gac gag ggt gcc gcc cag ggc gac gac gac gtc tgg Trp Asp Arg His Asp Glu Gly Ala Ala Gln Gly Asp Asp Asp Val Trp 385 390 395 400	1200
acc agc gga tcg gac tcc gac gaa gaa ctc gta acc acc gag cgc aag Thr Ser Gly Ser Asp Ser Asp Glu Glu Leu Val Thr Thr Glu Arg Lys 405 410 415	1248
acg ccc cgc gtc acc ggc ggc ggc gcc atg gcg ggc gcc tcc act tcc Thr Pro Arg Val Thr Gly Gly Gly Ala Met Ala Gly Ala Ser Thr Ser 420 425 430	1296

gcg ggc cgc aaa cgc aaa tca gca tcc tcg gcg acg gcg tgc acg tcg 1344
 Ala Gly Arg Lys Arg Lys Ser Ala Ser Ser Ala Thr Ala Cys Thr Ser
 435 440 445

 ggc gtt atg aca cgc ggc cgc ctt aag gcc gag tcc acc gtc gcg ccc 1392
 Gly Val Met Thr Arg Gly Arg Leu Lys Ala Glu Ser Thr Val Ala Pro
 450 455 460

 gaa gag gac acc gac gag gat tcc gac aac gaa atc cac aat ccg gcc 1440
 Glu Glu Asp Thr Asp Glu Asp Ser Asp Asn Glu Ile His Asn Pro Ala
 465 470 475 480

 gtg ttc acc tgg ccg ccc tgg cag gcc ggc atc ctg gcc cgc aac ctg 1488
 Val Phe Thr Trp Pro Pro Trp Gln Ala Gly Ile Leu Ala Arg Asn Leu
 485 490 495

 gtg ccc atg gtg gct acg gtt cag ggt cag aat ctg aag tac cag gaa 1536
 Val Pro Met Val Ala Thr Val Gln Gly Gln Asn Leu Lys Tyr Gln Glu
 500 505 510

 ttc ttc tgg gac gcc aac gac atc tac cgc atc ttc gcc gaa ttg gaa 1584
 Phe Phe Trp Asp Ala Asn Asp Ile Tyr Arg Ile Phe Ala Glu Leu Glu
 515 520 525

 ggc gta tgg cag ccc gct gcg caa ccc aaa cgt cgc cgc cac cgg caa 1632
 Gly Val Trp Gln Pro Ala Ala Gln Pro Lys Arg Arg Arg His Arg Gln
 530 535 540

 gac gcc ttg ccc ggg cca tgc atc gcc tcg acg ccc aaa aag cac cga 1680
 Asp Ala Leu Pro Gly Pro Cys Ile Ala Ser Thr Pro Lys Lys His Arg
 545 550 555 560

 ggt tga 1686
 Gly

<210> 14
 <211> 561
 <212> PRT
 <213> Human cytomegalovirus

<400> 14
 Met Glu Ser Arg Gly Arg Arg Cys Pro Glu Met Ile Ser Val Leu Gly
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 Pro Ile Ser Gly His Val Leu Lys Ala Val Phe Ser Arg Gly Asp Thr
 20 25 30
 Pro Val Leu Pro His Glu Thr Arg Leu Leu Gln Thr Gly Ile His Val
 35 40 45
 Arg Val Ser Gln Pro Ser Leu Ile Leu Val Ser Gln Tyr Thr Pro Asp
 50 55 60
 Ser Thr Pro Cys His Arg Gly Asp Asn Gln Leu Gln Val Gln His Thr
 65 70 75 80
 Tyr Phe Thr Gly Ser Glu Val Glu Asn Val Ser Val Asn Val His Asn
 85 90 95
 Pro Thr Gly Arg Ser Ile Cys Pro Ser Gln Glu Pro Met Ser Ile Tyr
 100 105 110

Val	Tyr	Ala	Leu	Pro	Leu	Lys	Met	Leu	Asn	Ile	Pro	Ser	Ile	Asn	Val	115	120	125
His	His	Tyr	Pro	Ser	Ala	Ala	Glu	Arg	Lys	His	Arg	His	Leu	Pro	Val	130	135	140
Ala	Asp	Ala	Val	Ile	His	Ala	Ser	Gly	Lys	Gln	Met	Trp	Gln	Ala	Arg	145	150	155
Leu	Thr	Val	Ser	Gly	Leu	Ala	Trp	Thr	Arg	Gln	Gln	Asn	Gln	Trp	Lys	165	170	175
Glu	Pro	Asp	Val	Tyr	Tyr	Thr	Ser	Ala	Phe	Val	Phe	Pro	Thr	Lys	Asp	180	185	190
Val	Ala	Leu	Arg	His	Val	Val	Cys	Ala	His	Glu	Leu	Val	Cys	Ser	Met	195	200	205
Glu	Asn	Thr	Arg	Ala	Thr	Lys	Met	Gln	Val	Ile	Gly	Asp	Gln	Tyr	Val	210	215	220
Lys	Val	Tyr	Leu	Glu	Ser	Phe	Cys	Glu	Asp	Val	Pro	Ser	Gly	Lys	Leu	225	230	235
Phe	Met	His	Val	Thr	Leu	Gly	Ser	Asp	Val	Glu	Glu	Asp	Leu	Thr	Met	245	250	255
Thr	Arg	Asn	Pro	Gln	Pro	Phe	Met	Arg	Pro	His	Glu	Arg	Asn	Gly	Phe	260	265	270
Thr	Val	Leu	Cys	Pro	Lys	Asn	Met	Ile	Ile	Lys	Pro	Gly	Lys	Ile	Ser	275	280	285
His	Ile	Met	Leu	Asp	Val	Ala	Phe	Thr	Ser	His	Glu	His	Phe	Gly	Leu	290	295	300
Leu	Cys	Pro	Lys	Ser	Ile	Pro	Gly	Leu	Ser	Ile	Ser	Gly	Asn	Leu	Leu	305	310	315
Met	Asn	Gly	Gln	Gln	Ile	Phe	Leu	Glu	Val	Gln	Ala	Ile	Arg	Glu	Thr	325	330	335
Val	Glu	Leu	Arg	Gln	Tyr	Asp	Pro	Val	Ala	Ala	Leu	Phe	Phe	Phe	Asp	340	345	350
Ile	Asp	Leu	Leu	Leu	Gln	Arg	Gly	Pro	Gln	Tyr	Ser	Glu	His	Pro	Thr	355	360	365
Phe	Thr	Ser	Gln	Tyr	Arg	Ile	Gln	Gly	Lys	Leu	Glu	Tyr	Arg	His	Thr	370	375	380
Trp	Asp	Arg	His	Asp	Glu	Gly	Ala	Ala	Gln	Gly	Asp	Asp	Asp	Val	Trp	385	390	395
Thr	Ser	Gly	Ser	Asp	Ser	Asp	Glu	Glu	Leu	Val	Thr	Thr	Glu	Arg	Lys	405	410	415
Thr	Pro	Arg	Val	Thr	Gly	Gly	Gly	Ala	Met	Ala	Gly	Ala	Ser	Thr	Ser	420	425	430
Ala	Gly	Arg	Lys	Arg	Lys	Ser	Ala	Ser	Ser	Ala	Thr	Ala	Cys	Thr	Ser	435	440	445
Gly	Val	Met	Thr	Arg	Gly	Arg	Leu	Lys	Ala	Glu	Ser	Thr	Val	Ala	Pro	450	455	460
Glu	Glu	Asp	Thr	Asp	Glu	Asp	Ser	Asp	Asn	Glu	Ile	His	Asn	Pro	Ala	465	470	475
Val	Phe	Thr	Trp	Pro	Pro	Trp	Gln	Ala	Gly	Ile	Leu	Ala	Arg	Asn	Leu	485	490	495
Val	Pro	Met	Val	Ala	Thr	Val	Gln	Gly	Gln	Asn	Leu	Lys	Tyr	Gln	Glu	500	505	510
Phe	Phe	Trp	Asp	Ala	Asn	Asp	Ile	Tyr	Arg	Ile	Phe	Ala	Glu	Leu	Glu	515	520	525
Gly	Val	Trp	Gln	Pro	Ala	Ala	Gln	Pro	Lys	Arg	Arg	Arg	His	Arg	Gln	530	535	540
Asp	Ala	Leu	Pro	Gly	Pro	Cys	Ile	Ala	Ser	Thr	Pro	Lys	Lys	His	Arg	545	550	555
Gly																		560

<210> 15
 <211> 3147
 <212> DNA
 <213> Human cytomegalovirus

<220>
 <221> CDS
 <222> (1)...(3144)

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gtc aac ttt ctg cgc cat ctc acg caa aag ccc gac gtg gat ctc gag 96
 Val Asn Phe Leu Arg His Leu Thr Gln Lys Pro Asp Val Asp Leu Glu
 20 25 30

gca cac ccc aag atc ctg aaa aaa tgt ggc gaa aaa cgc ctg cac cgg 144
 Ala His Pro Lys Ile Leu Lys Lys Cys Gly Glu Lys Arg Leu His Arg
 35 40 45

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 Arg Thr Val Leu Phe Asn Glu Leu Met Leu Trp Leu Gly Tyr Tyr Arg
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gag ctg cgt ttt cac aac ccc gac ctc tcc tca gtg ctc gag gag ttc 240
 Glu Leu Arg Phe His Asn Pro Asp Leu Ser Ser Val Leu Glu Glu Phe
 65 70 75 80

gag gtg cgt tgc gtg gcc gtg gcg cgt cgc ggc tac act tac ccg ttc 288
 Glu Val Arg Cys Val Ala Val Ala Arg Arg Gly Tyr Thr Tyr Pro Phe
 85 90 95

ggg gat cgt ggt aag gcg cgt gac cac ctg gct gtg cta gac cgt acc 336
 Gly Asp Arg Gly Lys Ala Arg Asp His Leu Ala Val Leu Asp Arg Thr
 100 105 110

gaa ttc gat acg gac gtg cgc cac gat gcc gag atc gtg gaa cgc gcg 384
 Glu Phe Asp Thr Asp Val Arg His Asp Ala Glu Ile Val Glu Arg Ala
 115 120 125

ctc gta agc gcg gtc att ctg gcc aag atg tcg gtg cgc gag acg ctg 432
 Leu Val Ser Ala Val Ile Leu Ala Lys Met Ser Val Arg Glu Thr Leu
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gtc aca gcc atc ggc cag acg gaa ccc atc gcc ttt gtg cac ctc aag 480
 Val Thr Ala Ile Gly Gln Thr Glu Pro Ile Ala Phe Val His Leu Lys
 145 150 155 160

gat acg gag gtg cag cgc att gaa gaa aac ctg gag ggt gtg cgc cgt 528
 Asp Thr Glu Val Gln Arg Ile Glu Glu Asn Leu Glu Gly Val Arg Arg
 165 170 175

aac atg ttc tgc gtg aaa ccg ctc gac ctt aac ctg gac cgg cac gcc 576

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aac	acg	gcg	ctg	gtc	aac	gcc	gtc	aac	aag	ctc	gtg	tac	acg	ggc	cgt	624
Asn	Thr	Ala	Leu	Val	Asn	Ala	Val	Asn	Lys	Leu	Val	Tyr	Thr	Gly	Arg	
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Leu	Ile	Met	Asn	Val	Arg	Arg	Ser	Trp	Glu	Glu	Leu	Glu	Arg	Lys	Cys	
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Met	Cys	Leu	Ser	Phe	Asp	Ser	Asn	Tyr	Cys	Arg	Asn	Ile	Leu	Lys	His	
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gcc	gtg	gaa	aac	ggc	gac	tcg	gcc	gac	acg	ctg	ttg	gag	ctg	ctc	atc	816
Ala	Val	Glu	Asn	Gly	Asp	Ser	Ala	Asp	Thr	Leu	Leu	Glu	Leu	Leu	Ile	
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Glu	Asp	Phe	Asp	Ile	Tyr	Val	Asp	Ser	Phe	Pro	Gln	Ser	Ala	His	Thr	
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Phe	Leu	Gly	Ala	Arg	Ser	Pro	Ser	Leu	Glu	Phe	Asp	Asp	Asp	Ala	Asn	
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Leu	Leu	Ser	Leu	Gly	Gly	Gly	Ser	Ala	Phe	Ser	Ser	Val	Pro	Lys	Lys	
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His	Val	Pro	Thr	Gln	Pro	Leu	Asp	Gly	Trp	Ser	Trp	Ile	Ala	Ser	Pro	
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Trp	Lys	Gly	His	Lys	Pro	Phe	Arg	Phe	Glu	Ala	His	Gly	Ser	Leu	Ala	
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Pro	Ala	Ala	Glu	Ala	His	Ala	Ala	Arg	Ser	Ala	Ala	Val	Gly	Tyr	Tyr	
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Gln	Asn	Leu	Gln	Gln	Arg	Gln	Gln	Gln	Pro	Pro	Pro	Pro	Ala	Arg	Lys	

405								410				415					
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Pro	Ser	Ala	Ser	Arg	Arg	Leu	Phe	Gly	Ser	Ser	Ala	Asp	Glu	Asp	Asp		
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Asp	Asp	Asp	Asp	Asp	Glu	Lys	Asn	Ile	Phe	Thr	Pro	Ile	Lys	Lys	Pro		
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Phe	Ser	Gly	Leu	Leu	Ser	Ser	Gly	Ser	Gln	Lys	Pro	Thr	Ser	Gly	Pro		
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Leu	Asn	Ile	Pro	Gln	Gln	Gln	Gln	Arg	His	Ala	Ala	Phe	Ser	Leu	Val		
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Ala	Trp	Asp	Val	Arg	Pro	Leu	Thr	Glu	Thr	Arg	Gly	Asp	Leu	Phe	Ser		
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Ser	Ala	Lys	Pro	Pro	Val	Thr	Thr	Ala	Tyr	Lys	Phe	Glu	Gln	Pro	Thr		
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Ile	Leu	Thr	Pro	Thr	Pro	Val	Asn	Pro	Ser	Thr	Ala	Pro	Ala	Pro	Ala		
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Trp Pro Arg Glu Arg Ala Trp Ala Leu Lys Asn Pro His Leu Ala Tyr	
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aca gcg tct cgg gac gcc gct gat gag gtt tgg gct tta agg gac caa	2112
Thr Ala Ser Arg Asp Ala Ala Asp Glu Val Trp Ala Leu Arg Asp Gln	
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act gca gag tca ccg gtc gaa gac agc gag gag gaa gac gac gac tcc	2160
Thr Ala Glu Ser Pro Val Glu Asp Ser Glu Glu Glu Asp Asp Asp Ser	
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Asp Tyr Asn Asn Asp Val Ile Ser Pro Pro Ser Gln Thr Pro Glu Gln	
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Pro Ala Lys Ser Ala Pro Pro Ser Pro Val Lys Gly Arg Gly Ser Arg	
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Val Gly Val Pro Ser Leu Lys Pro Thr Leu Gly Gly Lys Ala Val Val	
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Val Lys Ser Thr Thr Gly Met Lys Thr Val Ala Phe Asp Leu Ser Ser	
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ccc cag aag agc ggt acg ggg ccg caa ccg ggt tct gcc ggc atg ggg	3072
Pro Gln Lys Ser Gly Thr Gly Pro Gln Pro Gly Ser Ala Gly Met Gly	
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Gly Ala Lys Thr Pro Ser Asp Ala Val Gln Asn Ile Leu Gln Lys Ile	
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Glu	Val	Arg	Cys	Val	Ala	Val	Ala	Arg	Arg	Gly	Tyr	Thr	Tyr	Pro	Phe
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Gly	Asp	Arg	Gly	Lys	Ala	Arg	Asp	His	Leu	Ala	Val	Leu	Asp	Arg	Thr
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Ala	Pro	Pro	Val	Ala	Ser	Pro	Ser	Ile	Leu	Lys	Pro	Gly	Ala	Ser	Ala
965						970						975			
Ala	Leu	Gln	Ser	Arg	Arg	Ser	Thr	Gly	Thr	Ala	Ala	Val	Gly	Ser	Pro
980						985						990			
Val	Lys	Ser	Thr	Thr	Gly	Met	Lys	Thr	Val	Ala	Phe	Asp	Leu	Ser	Ser
995						1000						1005			
Pro	Gln	Lys	Ser	Gly	Thr	Gly	Pro	Gln	Pro	Gly	Ser	Ala	Gly	Met	Gly
1010						1015						1020			
Gly	Ala	Lys	Thr	Pro	Ser	Asp	Ala	Val	Gln	Asn	Ile	Leu	Gln	Lys	Ile
1025						1030						1035			
Glu	Lys	Ile	Lys	Asn	Thr	Glu	Glu								
1045															